

OM protein - protein search, using sw model

OM protein February 22, 2001, 18:19:54 ; Search time 12.32 Seconds
Run on: (without alignments)
996.084 Million cell updates/sec

US-09-316-080-2
2050

Sequence: 1 MENPTEYELNISVKLLE.....

Scoring table: BROSOMEZ
Gapop 10.0 , Gapext 0.5

Searched: 8875/ segs, 000000-
 -files chosen parameters: 8875

Minimum	DB seq	length:	0
Maximum	DB seq	length:	20000000000

post-processing: Minimum Match 08
Maximum Match 1008

Database : SwisProt_39:*

pred. No. is the number of results predicted by chance score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2025.5	98.8	383	1	TR15_GIBPU	P27679 gibberella
2	1966.5	95.9	377	1	TR15_FUSPO	O00835 fusarium po
3	1941	94.7	374	1	TR15_FUSBP	P13513 fusarium sp
4	1869.5	91.2	375	1	TR15_GIBBE	O00909 gibberella
5	1554	75.8	383	1	TR15_STACH	O59947 stachybotry
6	1525	74.4	385	1	TR15_MYRRO	O13469 myrothecium
7	136	6.6	1157	1	POL_STV31L	P27401 simian foam
8	101.5	5.0	728	1	UVRC_STRCO	G92512 streptomyces
9	100.5	4.9	804	1	SCY1_YEAST	P33009 saccharomyces
10	97.5	4.8	346	1	YCN1_ECOLI	P16228 escherichia
11	96	4.7	1162	1	BXEN_CLOBO	P46028 clostridium
12	96	4.7	1651	1	VITE_CAEEL	P18948 caenorhabdit
13	94.5	4.6	602	1	PEEP_LACLA	P11876 lactococcus
14	94	4.6	3660	1	DMD_CHICK	P11533 gallus gall
15	93	4.5	1666	1	CLH_SCHPO	O10161 schistosomach
16	92.5	4.5	855	1	MOTS_AOUPY	P10755 aequi-fex pyr
17	92	4.5	444	1	FDEF1_YEAST	P29704 saccharomyces
18	92	4.5	918	1	PEP3_YEAST	P27801 saccharomyces
19	92	4.5	971	1	VZ28_BOXBU	O51246 borrelia bu
20	91.5	4.5	626	1	PEPO_LACLA	O07744 lactococcus
21	91.5	4.5	880	1	ARG2_YEAST	P05085 saccharomyces
22	91	4.4	517	1	EUG1_YEAST	P32474 saccharomyces
23	91	4.4	761	1	VPA_BPP2	O06415 bacteriophaga
24	90.5	4.4	626	1	PEPO_LACEL	O08915 lactococcus
25	90.5	4.4	1469	1	DP27_CAEEL	P48996 caenorhabdit
26	90.5	4.4	3038	1	TRIO_HUMAN	P18592 homo sapiens
27	90	4.4	613	1	WA2_ACEAT	O06366 clostridium
28	89.5	4.4	765	1	VARA_BENTU	G38617 acetabularia
29	89.5	4.4	633	1	AMOR_BENTU	O39444 beta vulgaris
30	89	4.3	601	1	PEP1_LACLA	P15699 emericella
31	88.5	4.3	2184	1	RRPL_CVOO	P54121 lactococcus
32	88.5	4.3	2415	1	SPCA_DROME	P24658 canine dist
33	88	4.3	2415	1		P13395 drosophila

Q81115	caenorhabd1
P38827	saccharomyc
P56785	arabidopsis
P27195	flavobacter
P89430	herpes simp
P94954	methanopyru
Q38676	acetabularia
P47319	mycoplasma
O27552	methanobact
Q00963	drosophila
P49454	homo sapien
O26156	methanobact

ALIGNMENTS

ID	TRIS_GIBPU	STANDARD:	PRT:	383 AA.
RD	P26769;			
CC	01-AUG-1992 (Rel. 23, Created)			
CC	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	TRICHODIENE SYNTHASE (EC 4.1.99.6) (SESDOTITERPENE CYCLASE) (TS).			
OC	TRIS OR TOXS.			
OS	Gibberella pulicaris.			
OC	Eukaryota; Fungi; Ascomycota; Hypocreales; Nectriaceae; Gibberella.			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RP	MEDLINE=93043495; Pubmed=1421511;			
RT	Hohn T.M., Deejardins A.E.;			
RT	"Isolation and gene disruption of the Tox5 gene encoding trichodiene synthase in Gibberella pulicaris."			
RL	Mol. Plant Microbe Interact. 5:249-256(1992)			
CC	-1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.			
CC	IT CATALYSES THE ISOMERIZATION AND CYCLIZATION OF FARNESTYL PYROPHOSPHATE TO FORM TRICHODIENE, THE FIRST CYCLIC INTERMEDIATE IN THE BIOSYNTHETIC PATHWAY FOR TRICHOTHECENES. IT SERVES TO BRANCH THE BIOSYNTHETIC PATHWAY FROM THE ISOEPORENOL PATHWAY.			
CC	TRICHOTHECENE BIOSYNTHESIS FROM THE ISOEPORENOL DIPOSPHATE -			
CC	-1- CATALYTIC ACTIVITY: 2-TRANS,6-TRANS-FARNESYL DIPHOSPHATE -			
CC	TRICHODIENE + PYROPHOSPHATE,			
CC	-1- PATHWAY: TRICHOTHECENE BIOSYNTHESIS. TRICHOTHECENES ARE			
CC	SESDOTITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN			
CC	BIOSYNTHESIS.			
CC	-----			
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	or send an email to license@sdb.slb.ch .			
CC	-----			
DR	EMBL; M64348; AB203038.1;			
KW	LYASE.			
SV	SEQUENCE 383 AA; 44958 MW; ABB08F0BCB662P6 CRC64;			

Query Match	Score	Pred. No.	Indels	Gaps
Best Local Similarity	98.8%	4e-150	0	3
Matches	376	Conservative	4	Mismatches

121 RECAHPWALVNEHEPNVLRHGFPCSLNLTSTLDFECCNIEQVYNGGFPSMDI FAF 200

DB 121 RQAHFPMALVNEHPNVLNHFPGFCSLNLIRSTLDFEBCGTEIOYNGFGPSHDYPOF 180
 QY 181 LRRANGLGHCVCASLMPKQFDERGLFLEITSAIQMNNMVMVNDLMSFYKEPDERDQ 240
 DB 181 LRRANGLGHCVCASLMPKQFDERGLFLEITSAIQMNNMVMVNDLMSFYKEPDERDQ 240
 QY 241 ISLVNRYVVSDEITLHEALEKLTQDTLHSSKQMAVAFSDKDPQVMDTTECFMHCYVTHL 300
 DB 241 ISLVNRYVVSDEITLHEALEKLTQDTLHSSKQMAVAFSEKDPQVMDTTECFMHCYVTHL 300
 QY 301 CDHRRLNIEYKVGOKTEADQKCFKFEQAAVAVGAVSPSEMAVPPVLAOLANIRSKDV 359
 DB 301 CDHRRLNIEYKVGOKTEADQKCFKFEQAAVAVGAVSPSEMAVPPVLAOLANIRSKDV 360
 QY 360 --KDVAVEIKPILSLSTEIVE 380
 DB 361 DKAVKDLKIEKPLSLSTEIVE 383

RESULT 2

TRIS_FUSPO STANDARD: PRT: 377 AA.
 000835;

DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TRICHODIENE SYNTHASE (EC 4.1.99.6) (SESQUITERPENE CYCLASE) (TS).
 GN TRIS OR TOX5.
 OS Fusarium poae.
 OC Eukaryota; Fungi; Ascomycota; amorphous Ascomycota; Fusarium.
 RN [1]
 RP MEDLINE-98095652; PubMed-9433809;
 RA Fekete C., Logrieco A., Glacey G., Hornok L.;
 RT Screening of fungi for the presence of the trichodiene synthase
 RT encoding sequence by hybridization to the tris gene cloned from
 RT Fusarium poae.
 RL Mycopathologia 138:91-97(1997).
 CC -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
 CC IT CATALYZES THE ISOMERIZATION AND CYCLIZATION OF FARNESYL PYRO-
 CC PHOSPHATE TO FORM TRICHODIENE, THE FIRST CYCLIC INTERMEDIATE IN
 CC THE BIOSYNTHETIC PATHWAY FOR TRICHOTECENES. IT SERVES TO BRANCH
 CC TRICHOTECENE BIOSYNTHESIS FROM THE ISOPRENOID PATHWAY.
 CC CATALYTIC ACTIVITY: 2-TRANS, 6-TRANS-FARNESYL DIPHOSPHATE -
 CC TRICHODIENE + PYROPHOSPHATE.
 CC -1- PATHWAY: TRICHOTECENE BIOSYNTHESIS. TRICHOTECENES ARE
 CC SESQUITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN
 CC BIOSYNTHESIS.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: U15658; AAA50765.1.
 DR Lyase.
 KM
 SO SEQUENCE 377 AA: 44157 MW: 8483DF3CB730F6AB CRC64;

Query Match 95.9%; Score 1966.5; DB 1; Length 377;
 Best Local Similarity 96.3%; Pred. No. 1.5e-145;
 Matches 366; Conservative 6; Mismatches 5; Indels 3; Gaps 1;

QY 1 MENPTEFLNTSVRLLEYIRYRDSNTTREERINLHYAVNKAHHAFAPOROOQLKAVDP 60
 DB 1 MENPTEFLNTSVRLLEYIRYRDSNTTREERINLHYAVNKAHHAFAPOROOQLKAVDP 60
 QY 61 KRLQASLQITVGVVYVSAKVKSCADLSITHTTVLVLDSSDDPYFAMANYFNDLQAG 120
 DB 61 KRLQASLQITVGVVYVSAKVKSCADLSITHTTVLVLDSSDDPYFAMANYFNDLQAG 120

QY 121 RQAHFPMALVNEHPNVLNHFPGFCSLNLIRSTLDFEBCGTEIOYNGFGPSHDYPOF 180
 DB 121 RQAHFPMALVNEHPNVLNHFPGFCSLNLIRSTLDFEBCGTEIOYNGFGPSHDYPOF 180
 QY 181 LRRANGLGHCVCASLMPKQFDERGLFLEITSAIQMNNMVMVNDLMSFYKEPDERDQ 240
 DB 181 LRRANGLGHCVCASLMPKQFDERGLFLEITSAIQMNNMVMVNDLMSFYKEPDERDQ 240
 QY 241 ISLVNRYVVSDEITLHEALEKLTQDTLHSSKQMAVAFSDKDPQVMDTTECFMHCYVTHL 300
 DB 241 ISLVNRYVVSDEITLHEALEKLTQDTLHSSKQMAVAFSEKDPQVMDTTECFMHCYVTHL 300
 QY 301 CDHRRLNIEYKVGOKTEADQKCFKFEQAAVAVGAVSPSEMAVPPVLAOLANIRSKDV 360
 DB 301 CDHRRLNIEYKVGOKTEADQKCFKFEQAAVAVGAVSPSEMAVPPVLAOLANIRSKDV 360
 QY 361 DKAVKDLKIEKPLSLSTEIVE 380
 DB 361 DKAVKDLKIEKPLSLSTEIVE 383

RESULT 3

TRIS_FUSPP STANDARD: PRT: 374 AA.
 ID TRIS_FUSPP

DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TRICHODIENE SYNTHASE (EC 4.1.99.6) (SESQUITERPENE CYCLASE) (TS).
 GN TRIS OR TOX 5.
 OS Fusarium sporotrichoides.
 OC Eukaryota; Fungi; Ascomycota; amorphous Ascomycota; Fusarium.
 RN [1]
 RP MEDLINE-89378769; PubMed-2777086;
 RA Bohn T.M., Beremand P.D.;
 RT Isolation and nucleotide sequence of a sesquiterpene cyclase gene
 RT from the trichothecene-producing fungus Fusarium sporotrichoides.
 RL Gene 79:131-138(1989).
 CC -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
 CC IT CATALYZES THE ISOMERIZATION AND CYCLIZATION OF FARNESYL PYRO-
 CC PHOSPHATE TO FORM TRICHODIENE, THE FIRST CYCLIC INTERMEDIATE IN
 CC THE BIOSYNTHETIC PATHWAY FOR TRICHOTECENES. IT SERVES TO BRANCH
 CC TRICHOTECENE BIOSYNTHESIS FROM THE ISOPRENOID PATHWAY.
 CC CATALYTIC ACTIVITY: 2-TRANS, 6-TRANS-FARNESYL DIPHOSPHATE -
 CC TRICHODIENE + PYROPHOSPHATE.
 CC -1- PATHWAY: TRICHOTECENE BIOSYNTHESIS. TRICHOTECENES ARE
 CC SESQUITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN
 CC BIOSYNTHESIS.
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 CC EMBL: M27246; M213657.1.
 DR PIR: J00064; SYFUTP.
 KM Lyase.
 SO SEQUENCE 374 AA: 43999 MW: 18988FC1663C3763 CRC64;

Query Match 94.7%; Score 1941; DB 1; Length 374;
 Best Local Similarity 94.2%; Pred. No. 1.4e-143;
 Matches 358; Conservative 10; Mismatches 6; Indels 6; Gaps 1;

QY 1 MENPTEFLNTSVRLLEYIRYRDSNTTREERINLHYAVNKAHHAFAPOROOQLKAVDP 60
 DB 1 MENPTEFLNTSVRLLEYIRYRDSNTTREERINLHYAVNKAHHAFAPOROOQLKAVDP 60

61 KRLQASLQTIYGVNYSWATVSKCNADISHTYTLVLDDSSDPYAMANTFNDLQAG 120
 61 KRLQASLQTIYGVNYSWATVSKCNADISHTYTLVLDDSSDPYAMANTFNDLQAG 120
 121 RQAHFMAALVNEHPNVLRFHGFPCSLNIRSTLDFEFGCITEQYNGGPGSHDYPQF 180
 121 RQAHFMAALVNEHPNVLRFHGFPCSLNIRSTLDFEFGCITEQYNGGPGSHDYPQF 180
 121 RQAHFMAALVNEHPNVLRFHGFPCSLNIRSTLDFEFGCITEQYNGGPGSHDYPQF 180
 181 LRRANGIGHCYVASLMPKPEQDEGLFLEITSAIAQENMMVWVNDLMSFYKEPDERDQ 240
 181 LRRANGIGHCYVASLMPKPEQDEGLFLEITSAIAQENMMVWVNDLMSFYKEPDERDQ 240
 241 ISLVKNTVSDDETLHEALEKLTQDTLHSSKOMAVASDPOVMOTIECFMNGYVWHL 300
 241 ISLVKNTVSDDETLHEALEKLTQDTLHSSKOMAVASDPOVMOTIECFMNGYVWHL 300
 301 CDHRTLNELTEYKQKTEADAKFCFEQANAVGAVSPSEMAVPPVQALANIRSKDYK 360
 301 CDHRTLNELTEYKQKTEADAKFCFEQANAVGAVSPSEMAVPPVQALANIRSKDYK 360
 361 DVKDYKEIQKPLSSIELVE 380
 357 --KDYKEIQKPLSSIELVE 374

RESULT 4
 ID TRIS_GIBZE STANDARD: PRT: 375 AA.

AC 000909; STRAIN-W-8; MEDLINE-96172749; Pubmed-8589414;
 RA Proctor R.H., Rohm T.M., McCormick S.P.;
 "Reduced virulence of *Gibberella* zea caused by disruption of a
 trichothecene toxin biosynthetic gene."
 RT trichothecene toxin biosynthetic gene. 8:993-601(1995).
 CC mol. Plant Microbe Interact. 8:993-601(1995).
 CC -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
 CC THE BIOSYNTHETIC PATHWAY FOR TRICHOECENES. IT SERVES TO BRANCH
 CC PROSPARATE TO FORM TRICHOECENES, THE FIRST CYCLIC INTERMEDIATE IN
 CC THE BIOSYNTHETIC PATHWAY FOR TRICHOECENES. IT SERVES TO BRANCH
 CC TRICHOECENE BIOSYNTHESIS FROM THE ISOPRENOL DIPHOSPHATE -
 CC CATALYTIC ACTIVITY: 2-TRANS-6-TRANS-FARNESYL DIPHOSPHATE -
 CC TRICHOECENE + PYROPHOSPHATE.
 CC TRICHOECENE BIOSYNTHESIS. TRICHOECENES ARE
 CC -1- PATHWAY: TRICHOECENE BIOSYNTHESIS. TRICHOECENES ARE
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 CC EMBL: 022464; AAB72033.1;
 DR Lyase. 375 AA; 43942 MW; 2224743B33FE218D CRC64;
 SO SEQUENCE

Query Match 91.2%; Score 1869.5; DB 1; Length 375;
 Best Local Similarity 90.8%; Pred. No. 5e-138;
 Matches 345; Conservative 17; Mismatches 13; Indels 5; Gaps 1;

1 MENPTEFLNTSVRLLEYIRYDSNTYREERIENTAHYANKAAHFAQROOQLATYDP 60
 1 MENPTEFLNTSVRLLEYIRYDSNTYREERIENTAHYANKAAHFAQROOQLATYDP 60
 61 KRLQASLQTIYGVNYSWATVSKCNADISHTYTLVLDDSSDPYAMANTFNDLQAG 120
 61 KRLQASLQTIYGVNYSWATVSKCNADISHTYTLVLDDSSDPYAMANTFNDLQAG 120
 121 RQAHFMAALVNEHPNVLRFHGFPCSLNIRSTLDFEFGCITEQYNGGPGSHDYPQF 180
 121 RQAHFMAALVNEHPNVLRFHGFPCSLNIRSTLDFEFGCITEQYNGGPGSHDYPQF 180
 121 RQAHFMAALVNEHPNVLRFHGFPCSLNIRSTLDFEFGCITEQYNGGPGSHDYPQF 180
 181 LRRANGIGHCYVASLMPKPEQDEGLFLEITSAIAQENMMVWVNDLMSFYKEPDERDQ 240
 181 LRRANGIGHCYVASLMPKPEQDEGLFLEITSAIAQENMMVWVNDLMSFYKEPDERDQ 240
 241 ISLVKNTVSDDETLHEALEKLTQDTLHSSKOMAVASDPOVMOTIECFMNGYVWHL 300
 241 ISLVKNTVSDDETLHEALEKLTQDTLHSSKOMAVASDPOVMOTIECFMNGYVWHL 300
 301 CDHRTLNELTEYKQKTEADAKFCFEQANAVGAVSPSEMAVPPVQALANIRSKDYK 360
 301 CDHRTLNELTEYKQKTEADAKFCFEQANAVGAVSPSEMAVPPVQALANIRSKDYK 360
 361 DVKDYKEIQKPLSSIELVE 380
 359 --DVKDYKEIQKPLSSIELVE 375

RESULT 5
 ID TRIS_STACH STANDARD: PRT: 383 AA.

AC 05947; STRAIN N.A.; Wong B.;
 RA Submitted (MAR-1998) to the EMBL/Genbank/DBU databases.
 CC -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
 CC IT CATALYZES THE ISOMERIZATION AND CYCLIZATION OF FARNESYL PYRO-
 CC PHOSPHATE TO FORM TRICHOECENES, THE FIRST CYCLIC INTERMEDIATE IN
 CC THE BIOSYNTHETIC PATHWAY FOR TRICHOECENES. IT SERVES TO BRANCH
 CC TRICHOECENE BIOSYNTHESIS FROM THE ISOPRENOL DIPHOSPHATE -
 CC CATALYTIC ACTIVITY: 2-TRANS-6-TRANS-FARNESYL DIPHOSPHATE -
 CC TRICHOECENE + PYROPHOSPHATE.
 CC TRICHOECENE BIOSYNTHESIS. TRICHOECENES ARE
 CC -1- PATHWAY: TRICHOECENE BIOSYNTHESIS. TRICHOECENES ARE
 CC BIOSYNTHESIS.
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 CC EMBL: AF053926; AAC12640.1;
 DR Lyase. 383 AA; 44988 MW; F311FA326F82EDC CRC64;
 SO SEQUENCE

Query Match 75.8%; Score 1554; DB 1; Length 383;
 Best Local Similarity 77.5%; Pred. No. 1.6e-113;
 Matches 282; Conservative 33; Mismatches 49; Indels 0; Gaps 0;

DB 1 MENPTEFLGTAIRLEENVKIRDSNRYREVENIQAAYNNAAHFOERQOOLIKVSP 60
 QY 61 KRLQASLQTIYGVWVYVSWAKVSKECNADLSIHYYTLVLDDSSDDPYPAMANNFNDLQ 120
 DB 61 KRLASLRTIYGVWVYVSWAKVSKELMADLSIHYYTLVLDDSSDDPYPAMANNFNDLQ 120
 QY 121 REQAHPMALVNEHPVNLRHFGPFCSLNIRSTLDFEFCGWIQYNGFGPSHDYPOF 180
 DB 121 REQHPMMLVNEHPVNLRHFGPFCSLNIRSTLDFEFCGWIQYNGFGPSHDYPOF 180
 QY 181 LRRANGHCHGASLMPKEQDERGLFLEITSAIAQENNNVNDLSFYKEFDEPQ 240
 DB 181 LRRANGHCHGASLMPKEQDERGLFLEITSAIAQENNNVNDLSFYKEFDEPQ 240
 QY 241 ISLVKNVYVSDITLHEALKEKLTODTLHSSKQAVAFSDKDPQVNDTIECFMHIYTHL 300
 DB 241 ISLVKNVYVSDITLHEALKEKLTODTLHSSKQAVAFSDKDPQVNDTIECFMHIYTHL 300
 QY 301 CDHRYRLKEIYKVGKGTEDAKCFKFEQAANVAVSPSEAVYPIAQLANIRSKDV 360
 DB 301 CDHRYRLKEIYKVGKGTEDAKCFKFEQAANVAVSPSEAVYPIAQLANIRSKDV 360
 QY 361 DYKD 364
 DB 361 AERD 364

RESULT 6
 ID TRIS MYRO STANDARD: PRT: 385 AA.

AC 013489: 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TRICHOIDESE SYNTHASE (EC 4.1.99.6) (SEQUITERPENE CYCLASE) (TS).
 GN TRIS.
 OS Myrothecium rostratum.
 OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Myrothecium.
 NM (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN-ATCC 52485;
 RX MEDLINE-98190320; PubMed-9529523;
 RA Trapp S.C., Hohn T.M., McCormick S., Jarvis B.B.;
 RT Characterization of the gene cluster for biosynthesis of macrocyclic
 trichothecenes in Myrothecium rostratum.
 RL Mol. Genet. 257:421-432(1998).
 CC -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
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 THE BIOSYNTHETIC PATHWAY FOR TRICHOIDESE. IT SERVES TO BRANCH
 TRICHOIDESE BIOSYNTHESIS FROM THE ISOPRENOID PATHWAY.
 CC CATALYTIC ACTIVITY: 2-TRANS-6-TRANS-FARNESYL DIPHOSPHATE -
 -1- PATHWAY: TRICHOIDESE BIOSYNTHESIS. TRICHOIDESE ARE
 SESQUITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN
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 CC EMBL: AF009416; AAC49957.1;
 DR Lysase.
 FM SEQUENCE 385 AA; 44869 MW; 25AA92729DSB0D66 CRC64;

Matches 282; Conservative 37; Mismatches 54; Indels 4; Gaps 1;
 QY 1 MENPTEFLGTAIRLEENVKIRDSNRYREVENIQAAYNNAAHFOERQOOLIKVSP 60
 DB 1 MENPTEFLGTAIRLEENVKIRDSNRYREVENIQAAYNNAAHFOERQOOLIKVSP 60
 QY 61 KRLQASLQTIYGVWVYVSWAKVSKECNADLSIHYYTLVLDDSSDDPYPAMANNFNDLQ 120
 DB 61 KRLASLRTIYGVWVYVSWAKVSKELMADLSIHYYTLVLDDSSDDPYPAMANNFNDLQ 120
 QY 121 REQAHPMALVNEHPVNLRHFGPFCSLNIRSTLDFEFCGWIQYNGFGPSHDYPOF 180
 DB 121 REQHPMMLVNEHPVNLRHFGPFCSLNIRSTLDFEFCGWIQYNGFGPSHDYPOF 180
 QY 181 LRRANGHCHGASLMPKEQDERGLFLEITSAIAQENNNVNDLSFYKEFDEPQ 240
 DB 181 LRRANGHCHGASLMPKEQDERGLFLEITSAIAQENNNVNDLSFYKEFDEPQ 240
 QY 241 ISLVKNVYVSDITLHEALKEKLTODTLHSSKQAVAFSDKDPQVNDTIECFMHIYTHL 300
 DB 241 ISLVKNVYVSDITLHEALKEKLTODTLHSSKQAVAFSDKDPQVNDTIECFMHIYTHL 300
 QY 301 CDHRYRLKEIYKVGKGTEDAKCFKFEQAANVAVSPSEAVYPIAQLANIRSKDV 360
 DB 301 CDHRYRLKEIYKVGKGTEDAKCFKFEQAANVAVSPSEAVYPIAQLANIRSKDV 360
 QY 361 DYKD 364
 DB 361 AERD 364

RESULT 7
 ID POL SFV3L STANDARD: PRT: 1157 AA.

AC P27401: 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE
 TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].
 GN POL.
 OS Simian foamy virus (type 3 / strain LK3) (SFV-3).
 OC Viruses; Retrovird viruses; Retroviridae; Spumaviridae.
 NM (1)
 RN SEQUENCE FROM N.A.
 RP MEDLINE-92124734; PubMed-1310187;
 RA Renne R., Friedl E., Schweizer M., Fleps U., Turek R.,
 RT Neumann-Haefelin D.;
 RT Genomic organization and expression of simian foamy virus type 3
 (SFV-3).
 RL Virology 186:597-608(1992).
 CC -1- P.TM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -1- MISCELLANEOUS: THIS POLYPROTEIN IS PROBABLY SYNTHESIZED AS A
 GAG-POL POLYPROTEIN BY A +1 FRAMESHIFT.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A9.
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 CC EMBL: M74895; AAA47796.1;
 DR PIR: B40820; GNLJIK.
 DR HSP: P04385; IRTI.
 DR MEROPS: A09.001;
 DR INTERPRO: IPR000477;
 DR INTERPRO: IPR001037;
 DR INTERPRO: IPR001641;
 DR INTERPRO: IPR002156;
 DR PFM: PF00552; Integrase; 1.

Query Match 74.48; Score 1525; DB 1; Length 385;
 Local Similarity 74.88; Pred. No. 2.8e-111;